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SEQUENCE FROM N.A.
RA TISSUE-LING CARINOMIA:
RA Strausberg R.: 2001) to the EMBL/GenBank/DBJ databases.
RA Submitted (Mar 2001) to the EMBL/GenBank/DBJ databases.
RA InterPro: IPR000874; Bombsin.
DR Pfam: PF02044; Bombsin; 1.
DR PROSITE: PS00257; Bombsin; 1.
SQ SEQUENCE 148 AA; 16213 MW; 6A9DE9E274825BD CRC64;

Query Match 16.3%; Score 92.5; DB 13; Length 146;
Best Local Similarity 32.8%; Pred. No. 0.46;
Matches 39; Conservative 13; Mismatches 27; Indels 37; Gaps 7;

OY 1 MGGSLHFALLAGVPLSMDELPEPSASAKT-----RVHSRQKLMATIGHFPGKKS 51
DB 1 MGGSLHFALLAGVPLSMDELPEPSASAKT-----RVHSRQKLMATIGHFPGKKS 54
OY 52 L-EPSSPFLCTAHTSLRQDL-----QLSHDLGLTLIK-----KALG 90
DB 55 TGESSYSERG-----SLKQRLREYIRMEBAKMLGLITLAKNNHNPQPKAKLG 105

RESULT 6
OY0253 PRELIMINARY: PRT; 119 AA.
AC 090253:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PHE-13 BOMBSIN PREPROHORMONE.
OC Bombina orientalis (Oriental fire-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OY NCBI_TaxID=8346;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96205965; PubMed=8631814;
RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,
RA Dong J.Z., Spindel E.R.;
RA "There are three distinct forms of bombsin. Identification of
RA Leu31bombsin, Phe31bombsin, and [Ser3,Arg10,Phe31]bombsin in
RA R. triol. Chem. 271:7731-7737(1996).
RA EMBL: U49450; AAC59784.1; -.
DR InterPro: IPR000874; Bombsin.
DR Pfam: PF02044; Bombsin; 1.
DR PROSITE: PS00257; Bombsin; 1.
DR CHAIN 45
FT CHAIN 119 AA; 13888 MW; 5C9BD03507441E59A CRC64;
SQ SEQUENCE 119 AA; 13888 MW; 5C9BD03507441E59A CRC64;

Query Match 15.0%; Score 85; DB 13; Length 119;
Best Local Similarity 27.0%; Pred. No. 0.48;
Matches 31; Conservative 19; Mismatches 49; Indels 16; Gaps 5;

OY 3 GSLHFALLAGVPLSMDELPEPSASAKTIRVHSRQKLMATIGHFPGKKSLEPSSPSP 59
DB 13 GFLHF--LIFSRFSLSCHEVVDNNQGLSLQSLQNLQNMVGHFPGKKSLEDDYDEE 70
OY 60 LGTAHTSLRQDLQSLSDGLILKAKAVLSLRPAQIO--VRLLVQTLQK 112
DB 71 MESFAKKNVEMNR-----AALLQBNRAESRELIKNVQLAVNMLIDYLRK 116

RESULT 7
OY0254 PRELIMINARY: PRT; 119 AA.
AC 090254:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE SAP BOMBSIN PREPROHORMONE.
OC Bombina orientalis (Oriental fire-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OY NCBI_TaxID=8346;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96205965; PubMed=8631814;
RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,
RA Dong J.Z., Spindel E.R.;
RA "There are three distinct forms of bombsin. Identification of
RA Leu31bombsin, Phe31bombsin, and [Ser3,Arg10,Phe31]bombsin in
RA R. triol. Chem. 271:7731-7737(1996).
RA EMBL: U49451; AAC59785.1; 27(1996).
DR InterPro: IPR000874; Bombsin.
DR Pfam: PF02044; Bombsin; 1.
DR PROSITE: PS00257; Bombsin; UNKNOWN.1.
DR CHAIN 45
FT CHAIN 119 AA; 13745 MW; 7F95C34EDB68702 CRC64;
SQ SEQUENCE 119 AA; 13745 MW; 7F95C34EDB68702 CRC64;

Query Match 13.5%; Score 76.5; DB 13; Length 119;
Best Local Similarity 30.3%; Pred. No. 0.46;
Matches 23; Conservative 13; Mismatches 35; Indels 5; Gaps 2;

OY 3 GSLHFALLAGVPLSMDELPEPSASAKTIRVHSRQKLMATIGHFPGKKSLEPSSPSP 59
DB 13 GFLHF--LIFSRFSLSCHEVVDNNQGLSLQSLQNLQNMVGHFPGKKSLEDDYDEE 70
OY 60 LGTAHTSLRQDLQSLSDGLILKAKAVLSLRPAQIO--VRLLVQTLQK 112
DB 71 MESFAKKNVEMNRAL 86

RESULT 8
OY0612 PRELIMINARY: PRT; 771 AA.
AC 096C12:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE HYPOHETICAL 81.4 KDa PROTEIN.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OY NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-SKIN, MELANOMA, AND HIGH MDR.
RA Strausberg R.: 2001) to the EMBL/GenBank/DBJ databases.
RA InterPro: IPR014945; AAH14945.1; -.
DR EMBL: BC014945; AAH14945.1; -.
KW Hypothetical protein.
SQ SEQUENCE 771 AA; 81368 MW; 98B3B052CD34191B CRC64;

Query Match 13.2%; Score 75; DB 4; Length 771;
Best Local Similarity 27.0%; Pred. No. 0.5;
Matches 32; Conservative 16; Mismatches 36; Indels 36; Gaps 6;

OY 2 FGSLLHFALLAGVPLSMDELPEPSASAKTIRVHSRQKLMATIGHFPGKKSLEPSSPSP 60
DB 423 YGALLAMLVAVVAPDDW--PAPRRAP--LISRR--ELDERILQNLIVQASPPGV 475
OY 61 GTPAFSLSD-----QRLQSLDGLILKAKAVLSLRPAQIO--VRLLVQTLQK 98
DB 476 GATHTLLSGSPDMVACALPTPTQRPFLMRLLLEGGLHLL-----AALPPRA 529

RESULT 9
OY9EV74 PRELIMINARY: PRT; 243 AA.
ID 09EV74

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AC Q9EV74: (TREMBL)rel_16, Created)
DT 01-MAR-2001 (TRENEMBL)rel_16, Last sequence update)
DR 01-MAR-2001 (TRENEMBL)rel_17, Last annotation update)
DE BPHS PROTEIN.
OS BPHS.
GN BPHS.
NC Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteriota; beta subdivision; Ralstonia group;
CC Ralstonia.
ID NCBI_TaxId=510:
LN 11
LN SOURCE FROM N.A.
LN STRAIN=A5: TRANSPOSON-TNA371:
RC MEDLINE=20092484; PubMed=10628682:
RX Moutz S., Merit C., Spinggaard D., Tousseau A.:
RA "Organization of the bph gene cluster of transposon Tna371, encoding enzymes for the degradation of biphenyl and 4-chlorobiphenyl compounds."
RT Mol. Gen. Genet. 253:499-506(1997).
RL 12
RP SEQUENCE FROM N.A.
RN 11
RS STRAIN=A5: TRANSPOSON-TNA371:
RC MEDLINE=20092484; PubMed=10628682:
RX Moutz S., Merit C., Spinggaard D., Tousseau A.:
RA "A GntR-like negative regulator of the biphenyl degradation genes of the transposon Tna371."
RL Mol. Gen. Genet. 262:790-799(1999).
RD EMBL: AB012252; FRODOJ524.LINK:
DR SMART: SM00345; HTHLNTR_1.
DS SEQUENCE 243 AA; 27190 MW; E90DBEAFCAZCFB2D CRC64:
QY Query Match 13.1%; Score 74.5; Db 2; Length 243;
Beat Local Similarity 34.8%; Pred. No. 1.6;
Matches 31; Conservative 31; Missmatches 31; Indels 15; Gaps 5
Db 13 VASG--WPGAGHGMNMGKRRRRPFOFSPVATLRDLICHLNGSHSGSRILAEITLK 67
OY 34 VHNSGKLALGHPN----GKRSLPPSSPPPLCGAAHRISLBODROLQH---DLGLTIILK 86
| 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 |
Db 13 VASG--WPGAGHGMNMGKRRRRPFOFSPVATLRDLICHLNGSHSGSRILAEITLK 67
OY 87 KALGVG---LSRFPAPOIOTGRRLVDLIOLIK 112
| 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 | 1 : 1 |
Db 68 SLGVGSSTLRALNLTVGGNDLVAVREOGK 96
Q9A589 RESULT
ID ID Q9A589 PRELIMINARY: PRT; 297 AA.
PT 01-JUN-2001 (TRENEMBL)rel_17, Created)
DT 01-JUN-2001 (TRENEMBL)rel_17, Last annotation update)
DE 01-DSC-2001 (TRENEMBL)rel_13, Last annotation update)
DE INTEGRAL MEMBRANE PROTEIN.
DE CC2568.
OS Caulobacter crescentius.
OC Bacteria; Proteobacteriota; alpha subdivision; Caulobacter group;
CC Caulobacter.
ID NCBI_TaxId=69394:
LN 11
LN SOURCE FROM N.A.
LN STRAIN=ATCC 19089 / GA15:
RC MEDLINE=21175688; PubMed=11259647:
RX Niemman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Madock J.B.,
RA Potocnik I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Dobay R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Heit D.H.,
RA Johnston A.P., Mile J., Meyers M., Baumhoef H., Shetty D.B., Berry K.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Davis M., White O.,
RA "Complete genome sequence of Caulobacter crescentium."
RT Proc. Natl. Acad. Sci. U.S.A. 99:4136-4141(2001).
RD EMBL: AF0005925; AAC24538.1:
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DR TRIG: CC568; -
 DR InterPro: IPR000620; DUF6.
 DR Pfam: PF00992; DUF6; 2.
 DR Complete proteome
 KW SOURCE: 297 AA; 31783 MW; 31EEDB9C5A44ACDA CMC64;
 50

Query Match 13.0%; Score 74; Db 16; Length 297;
 Best Local Similarity 23.0%; Pred.No.2; 25;
 Matches 31; Conservative 20; Mismatches 26; Indels 30; Gaps 7.

Oy 1 MOSLRHRLALAGVPLSDLPENRSKRIWISCKYLAIGH-----PQKSILEPS 56
 Db 35 LYAAVRNALPAVL----HLDPARPMRYRNVY-----GLMGSGNPALIPGPGFASNA 69
 Oy 57 PS---PIGTPTSTLDDORLOSLDILLGILL-----KKALCVSIS 94
 Db 90 ASVTGWG-VPEPTT-----LLSVTLIDIKMRHGDIALT 124

RESULT 11
 OPG672 PRELIMINARY; PRT; 577 AA.
 ID OPG672 AC OPG672
 DT 01-OCT-2000 (TEMBUREl, 15, Created)
 DT 01-OCT-2000 (TEMBUREl, 15, Last sequence update)
 DT 01-DEC-2001 (TEMBUREl, 19, Last annotation update)
 DE DNA PRIMERASE.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group:
 OC Xylella.
 NC NCBITaxId=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed20365717; PubMed-10910347;
 RE MEDLINE20365717; PubMed-10910347;
 RA Simpson A.J.G., Reinach F.C., Attupe P., Abreu F.A., Agencio M.,
 Alvarez R., Alves L.M.C., Ataya J.E., Balá G.S., Baptista C.S.,
 Barros M.H., Bonaccorsi E.D., Brizio S., Boye J.N., Blomes M.R.S.,
 Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carro H.,
 Colomito N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Melo C.M.,
 Coutinho L.T., Cristofani M.S., Dias-Neco E., Dosena C., El-Dorri H.,
 Franco J.S., Franco S.C., Franco M.C., Frohme M., Galán L.R.,
 Garlier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 Ho P.L., Hochetel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 Kligler J.E., Kutanev E.E., Lalgett P., Lambais M.R., Leite L.C.C.,
 Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 Machado M.A., Moreira A.M.B.N., Medeira H.M.F., Marino C.L.,
 Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.T.,
 Meunier M., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 Nhamit A Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 Paixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pasquero J.B.,
 Ouagallo R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 da Silva A.C.R., de Silva R.G., Santelli R.V., Sawasaki H.E.,
 da Silva A.C.R., de Silva A.M., da Silva F.R., Silva W.A.Jr.,
 da Silveira J.F., Taramelli F., Tuffi Bignardi U., Ventura J.A.,
 de Souza J., Terenzi L.F., Truffi Bignardi U., Tezari S., Teubano M.H.,
 Vailland H., Van Sluyt M.A., Verjovski-Almeida S., Vechiato A.L.,
 Zago M.A., Zatz M., Zelditch J.C., Zsembik J.C.;
 The genome sequence of the plant pathogen Xylella fastidiosa.
 Nature 406:151-159(2000).
 EMBL: AE003894; AF83240.1;
 DB: HSSP: Q9XMD0.1000;
 DR InterPro: IPR002266; TROPIN;
 DR Pfam: PF00253; ZNCHC;
 DR Pfam: PF01871; TOPPIN_1;
 DR Pfam: PF01875; TOPPIN_2;
 DR Pfam: PF02988; ZNF_CHCC; 1;
 DR ProDom: PD002988; ZNF_CHCC; 1;
 DR SMART: SM00493; TOPPIN_1;

| | | | | |
|------------------|--|--------------|--|-------------------------------|
| D6 | | 169 | GTAAGGATCTACGTCAGSRRHCRGACRFAAHNSNDIDFRJAPLSPSSGVMKIVYWHNNCKI- | 227 |
| Oy | | 54 | PSSRSFCTAPRTSLRN----- | LOLSIDDLGLLKALKVLSLRPAQIO 107 |
| D6 | | 228 | -----SPAWEQVIYVRDQGTARAFPLVMDMLSTFEANCGLYKEVLAA-- | -DMALLA 286 |
| Oy | | 102 | VARELVQLRL 112 | |
| D6 | | 281 | PRRLAVELDR 291 | |
| RESULT 15 | | | | |
| ID | Q15142. | PRELIMINARY: | PTT: 3638 AA. | |
| AD | Q15142. | | | |
| DC | Q15142. | | | |
| DT | 01-NOV-1996 (TEMBLRel. 01, Created) | | | |
| DF | 01-NOV-1996 (TEMBLRel. 01, Last annotation update) | | | |
| DE | 01-DIC-2001 (TEMBLRel. 19, Last annotation update) | | | |
| OS | PROK1 | | | |
| CS | PROK1 | | | |
| CC | Homo sapiens (human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OX | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| NCBI_Taxid=9606; | | | | |
| RN | [1] | | | |
| RF | SEQUENCE FROM N.A. | | | |
| RA | Kerr J.F., Hargrave D.L., Buxton V.J., Thompson S., Gamble Y., McCarthy A.B., | | | |
| RA | Ward C.J., Pearl B., Hughes J., Kennedy T.J., Kearney L.H., Higgs D.R., | | | |
| RA | Silome-Stanley J., Buckle V.J., Harris P.C., Koeflisma J.H., Spruit L.L., Searis J.J., | | | |
| RA | Reutcliffe P.J., Harris P.C., Koeflisma J.H., Spruit L.L., Searis J.J., | | | |
| RA | Dauvergne H.G., Peters D.J.M., Breunling M.H., Nellist M., | | | |
| RA | Brook-Carter P., Maheshwar M.M., Cordelleiro I., Santos H., Cabral P., | | | |
| RA | Sampson J.R., Jensen B., Hassell-Jensen A.T.W., | | | |
| RA | Nelson G., Oueland A.M.W., Busen B., Verhoeft S., Lindhout D., | | | |
| RA | van den Ouweland A.M.W., | | | |
| RT | "The poly cystic kidney disease 1 gene encodes a 14 kb transcript and | | | |
| RT | lies within a duplicated region on chromosome 16. The European | | | |
| RT | poly cystic kidney disease consortium [published erratum appears in | | | |
| RT | Cell 1994 Aug 26;78(4): following 724]" | | | |
| RL | Ceil 77:881-894(1994). | | | |
| RM | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RA | Burn T.C., Connors T.D., Dackowski M.R., Petry L.R., Van Raay T.J., | | | |
| RA | Burn T.C., Connors T.D., Dackowski M.R., Petry L.R., Van Raay T.J., | | | |
| RA | Milliholland J., Venet M., Miller G., Hakim R.M., Doggett N.A., | | | |
| RA | Landes G.M., Klingner K.W., Qian F., Onuchic L.F., Melnick T., | | | |
| RA | Germán G.G., | | | |
| RT | "Analysis of the genomic sequence for the autosomal dominant | | | |
| RT | poly cystic kidney disease (PKD) gene predicts the presence of a | | | |
| RT | coding region." repeat. The American PKD Consortium (APKD) | | | |
| RL | Hum Mol Genet. 4:375-382(1995). | | | |
| RM | EMBL: P38161. AAS59488.1;" | | | |
| RA | HSSP: P38161. 1BAR. | | | |
| DR | InterPro: IPRO01304, lectin.C | | | |
| DR | InterPro: IPRO01024, I42 | | | |
| DR | InterPro: IPRO01611, LR | | | |
| DR | InterPro: IPRO00463, LRCLterm | | | |
| DR | InterPro: IPRO00463, LRCLterm | | | |
| DR | InterPro: IPRO03591, LR LYF | | | |
| DR | InterPro: IPRO00434, PKD.1 | | | |
| DR | InterPro: IPRO00203, PKD_Cys_1rich | | | |
| DR | InterPro: IPRO00601, PKD_domain | | | |
| DR | InterPro: IPRO02859, Rev | | | |
| DR | Pfam: PF01829, GFS: 1 | | | |
| DR | Pfam: PF00520, lectin.C. 1 | | | |
| DR | Pfam: PF00520, lectin.C. 1 | | | |
| DR | Pfam: PF01463, LRRC1 | | | |
| DR | Pfam: PF01463, LRRC1 | | | |
| DR | Pfam: PF00801, PKD. 11 | | | |
| DR | Pfam: PF01777, PLAT. 1 | | | |
| DR | Pfam: PF02010, Rev: 1 | | | |

[illegible]

Search completed: May 30, 2002, 17:25:49
Job time: 124 sec